The 13th International Symposium on Integrated Field Science “Conservation and Utilization of Biodiversity"

The 13th International Symposium on Integrated Field Science

Conservation and Utilization of Biodiversity

Date: March 9-11, 2016

Venue:
Lecture House no.1, Amamiya Campus, Graduate School of Agricultural Science, Tohoku University, Sendai, Japan

Hosted by
Field Science Center, Graduate School of Agricultural Science, Tohoku University, Japan

Organizer:
Yoshihisa Suyama
Associate professor
Laboratory of Forest Ecology, FSC,
Graduate School of Agricultural Science, Tohoku University

Program

Thursday, March 10

Registration

9:30–

Opening remarks

9:45–9:50

Invited Presentations

9:50–10:20 **E. A. JAMES** (Royal Botanic Gardens Victoria, Australia)
The Application of Genetics in Balancing the Conservation and Utilisation of Biodiversity in Multi-Use Environments

10:20–10:50 **Hyeok Jae CHOI** (Changwon National University, Korea)
Conservation Activities on Korean Rare and Endemic Plants —with a special reference to the Korea National Arboretum

10:50-11:00: Coffee Break

11:00–11:30 **Gustavo Maruyama MORI** (Agência Paulista de Tecnologia dos ronegócios, Brazil)

Unveiling the Genetic Variation of the Western Hemisphere Mangrove Genus *Rhizophora*

11:30–12:00 **Yuji ISAGI** (Kyoto University, Japan)
Conservation Genetics with Information from NGS in the Bonin Islands, a UNESCO World Heritage Site

12:00–13:00: Lunch

13:00–13:30 **Natsuko Ito KONDO** (National Institute for Environmental Studies, Japan)
DNA Barcoding, Environmental DNA and an Ongoing Attempt of Detecting Biodiversity in Lake Kasumigaura

Oral Presentations

13:30–13:45 **Hiroshi TOMIMATSU** (Yamagata University, Japan)
Identifying Life-History Processes behind the Abundant-Center Distribution of a Forest Herb along a Latitudinal Gradient

13:45–14:00 **Masakazu N. AOKI** (Tohoku University, Japan)
Are the Epiphytic Animal Communities in the Sargassum Forests off the Pacific Coast of Miyagi Recovering from the Alteration Caused by the 2011 Tsunami?

14:00–14:15 **Chika TADA** (Tohoku University, Japan)
Decentralized Energy Production System by Anaerobic Digestion Using Organic Waste and Exhaust Heat

14:15–14:30 **Yoshihisa SUYAMA** (Tohoku University, Japan)
Single-Pollen Genotyping Using the Next-Generation Sequencing

14:30-15:00: Coffee Break

Poster Preview
15:00–15:30
Poster Presentations
15:30–16:30
Closing Remarks
16:30–16:35
Reception
18:00–

Poster Presentations

1. C. Yonezawa et al.	Tohoku University	Aerial Measurement of Radiation Dose Distribution on Grassland Area in Kawatabi Field Science Center
2. S. Hano & Y. Kanayama	Tohoku University	Basic Study for Increasing Functional Food Ingredients Content in Tomato Using Genetic Diversity
3. H. Nariyama & Y. Kanayama	Tohoku University	Study on the Regulation of Cell Division Potentially Involved in Fruit Size Diversity in Tomato
4. H. Ohira et al.	Fukushima University University of Tsukuba	Molecular Phylogenetic Analysis of Japanese Soil-dwelling Mundochthonius Pseudoscorpions (Pseudoscorpiones: Chthoniidae)
5. S.Takizawa et al.	Tohoku University The Japanese Society for the Promotion of Science, Japan	Pretreatment of Paper Sludge with Rumen Fluid to Enhance Biogas Production
6. M. Umetsu et al.	Tohoku University	Observation of the Electrode Surface Microbes in Microbial Fuel Cells
7. R.Tajima et al.	Tohoku University	Predicting Yield, Flowering and Harvesting Dates of Highbush Blueberry Using Temperature Data: a Case Study in Field Science Center of Tohoku University
8. M.Fushimi et al.	Tohoku University Forestry and Forest Product Research Institute The Hokkaido University Museum Hokkaido University	Local Genetic Differentiation within Rebun Island in Cypripedium macranthos var. rebunense Revealed by Genome-wide SNP Analysis Using MIG-seq
9. T. Kanno & Y. Suyama	Tohoku University	Population Genetic Analysis for Identifying Hybrid Origin of a Dwarf Bamboo Species in Sasaella
10. K. Fujita et al.	Tohoku University	Conservation Genetics of Three Endangered Species of the Genus Oxera in the South of New Caledonia
11. T. Tanno et al.	Tohoku University	Plant Paleogenetics with Plant Macro-Remains from the Last Glacial Maximum

The Application of Genetics in Balancing the Conservation and Utilisation of Biodiversity in Multi-Use Environments

E. A. JAMES

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Natural systems are under increasing environmental pressures from human-mediated modification and a changing climate. Understanding the influences on plant abundance and distribution can assist in the management of these systems. Many Australian regions are experiencing lower rainfall and higher temperatures that will make some habitats less suitable in the future for species that occur there now. The use of genetic techniques can assist in promoting the evolutionary processes essential for ecosystem function and the services ecosystems provide. I will provide examples of studies where genetic techniques have enable us to understand patterns of genetic diversity by identifying maternal lineages, differentiating between individuals and clone mates and accurately measuring differences in genetic variation between individuals, populations and species. In conjunction with field-based information, better understanding of the patterns of diversity is leading to integrated management plans designed to balance the multiple pressures imposed by our use of resources with the essential requirements for biodiversity conservation.

Conservation Activities on Korean Rare and Endemic Plants - with a Special Reference to the Korea National Arboretum

Hyeok Jae CHOI[1] and Sungwon SON[2]

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The current status of conservation activities on the Korean rare and endemic species was reviewed with a special reference to the Korea National Arboretum (KNA). In the Korean peninsula, there are 4,172 plant taxa including 360 endemics and 571 rare plants categorized at the national level by the IUCN criteria: EW 4, CR 112, EN 199, LC 70, and DD 112. The KNA has established various *in-* and *ex-situ* conservation programs in practice for GSPC goals since 2010. In order to improve the conservation activities, the KNA has managed specialized research projects as well as networking programs with other local governmental arboreta and NGOs in Korea. The main purposes of the research projects are to (1) survey, update, and evaluate the conservation and genetic status of Korean populations of rare endemic plants; (2) formulate an urgent conservation strategy; and (3) monitor the endangered populations based on the latest and accurate ecological and biological information. For the *ex-situ* conservation, the KNA has secured and propagated seeds and living collections of rare and endemic plants, and as a result, the KNA conserves about 70% of Korean rare plants as living collection and propagules. A total of nine conservation fences have been installed and monitored by the KNA as part of *in-situ* conservation. In addition, the KNA has carried out a re-introduction program for rare plants such as epiphytic orchids in natural habitats by developing propagation techniques with accurate genetic tags. The KNA also promotes training and international cooperation programs for the in- and *ex-situ* conservation activities for the East Asian biodiversity.

Unveiling the Genetic Variation of the Western Hemisphere Mangrove Genus *Rhizophora*

Gustavo Maruyama MORI[1,2,3], Mariana Vargas CRUZ[2], Stephanie Karenina BAJAY[2], Koji TAKAYAMA[4], Yu MATSUKI[5], Rafael Silva OLIVEIRA[6], Yoshihisa SUYAMA[5], Anete Pereira de SOUZA[2,6], Maria Imaculada ZUCCHI[1] and Tadashi KAJITA[7]

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Global climate changes (GCC) are alterations on the climate properties whose biological effects are unquestionable. Different organisms, however, differently respond to these changes and mangrove forests are projected to be one of the most influenced environments. Understanding how and to what extent mangrove species responded to past climate alterations may provide clues to the prediction of their responses to the current GCC. Currently, our main objective is to describe the genetic structure of *Rhizophora* species from the Western hemisphere. Our results show that the two recognized species from this hemisphere, *R. mangle* and *R. racemosa*, and their putative hybrid compose a more intricate species complex. Moreover, considering only *R. mangle*, which is widely distributed across this biogeographic region, we observed that the American continent is an incomplete barrier to gene flow whereas oceans may provide pathways for long distance dispersal. We also aim to couple this information with species distribution modelling and niche analyses to unveil the past demographic history of these *Rhizophora* species across their distribution range. This project is part of a comparative and multidisciplinary study that uses genetic, transcriptomic, ecophysiological and ecological niche analyses to unveil the role of climate and its related environmental factors in the evolution and ecology of mangrove species from the western hemisphere.

Conservation Genetics with Information from NGS in the Bonin Islands, a UNESCO World Heritage Site

Yuji ISAGI[1], Shingo KANEKO[2], Satoshi NARITA[1], Ayu NARITA[1], Haruko ANDO[1, 3], and Taketo KOMURA[1]

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[3]Center for Environmental Biology and Ecosystem Studies, National Institute for Environmental Studies, Japan

The Bonin (Ogasawara) Islands are typical oceanic islands, located in the North-Western Pacific, ca. 1,000 km south of the main Japanese Archipelago. The land is dominated mainly by dry forests and sclerophyllous shrublands, and more than 440 native vascular plant species, including 70% endemics, are growing. As for land snail, 90% of 100 recorded native species are endemic. Outstanding examples of ongoing evolutionary processes evidenced by high levels of endemism and speciation by adaptive radiation can be observed in the Bonin Islands. Because of the combination of the high levels of endemism and significant adaptive radiation, the Bonin Islands were designated as a World Natural Heritage in 2011. As is often the case with oceanic island ecosystems, the Bonin Islands had been disturbed by human activities such as deforestation and introduction of invasive alien species.

In order to construct rational and effective conservation measures, we have been trying to understand/monitor the current status of the biodiversity by using genetic information from NGS. Genetic analyses for plant and bird species endemic to the Bonin Islands uncovered genetic structure, existence of unknown wild plants, unexpected feeding habitat of endangered birds, etc.

DNA Barcoding, Environmental DNA and an Ongoing Attempt of Detecting Biodiversity in Lake Kasumigaura

Natsuko Ito KONDO[1], Megumi NAKAGAWA[1], Shin-ichiro MATSUZAKI[1], Ryuhei UENO[1], Kenzi TAKAMURA[1] and Hiroshi ITO[2]

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Freshwater ecosystem is small in scale on earth but biologically diverse. Human activities induce a number of threats such as habitat loss and alterations in water quality, and a massive decrease in the population of freshwater organism is now becoming a more serious issue than terrestrial and marine lives (WWF 2012). Since freshwater provides various ecosystem services, understanding ecosystem function and mechanism that maintain ecosystem services in freshwater is essential.

In Lake Kasumigaura, National Institute for Environmental Studies (NIES) has been monthly collecting data on biodiversity as well as on water quality for over 40 years. Lake Kasumigaura in the Kanto Plain is the second largest lake in Japan and located about 60km north from Tokyo. It provides abundant ecosystem services such as water resource and fisheries, but has been threatened by declining quality of water, emergence of blue green algae and invasion of alien species. Monitoring data of Kasumigaura is used to evaluate the effects of anthropogenic disturbance on the lake ecosystem. For biological monitoring, abundance of bacterioplankton, phytoplankton, zooplankton, benthos and fish was surveyed with morphological identification. Since morphological identification requires expertise in taxonomy and takes enormous time even for experts, keeping the resolution of identification, especially at a species level, has been the problem.

Recently developed DNA barcoding and analyses of environmental DNA (eDNA) is one solution to compensate for the difficulty in the current monitoring methods. eDNA is a generic term for DNA extracted from environmental samples such as water and soils that contain DNA from whole bodies of tiny organisms and secretion or tissue fragments of larger organisms. To detect biodiversity in the lake, we evaluated the possibility to use DNA sequences from eDNA samples of the lake. For the reference of sequences from eDNA, sequence database of COI, a standard region of DNA barcoding for animals, has been built on fish, chironomids, and zooplankton of Lake Kasumigaura. We analyzed the COI fragment from eDNA amplified with animal universal primers by next generation sequencer and found that the resolution of biodiversity is high enough for zooplankton, but insufficient for larger organisms such as benthos and fish. The effect of filtration on detected sequence diversity and the importance of database were also indicated. For practical use of eDNA for a long-term monitoring in the lake, improvement of laboratory protocols will be discussed.

Reference:

WWF (2012) Living planet report –Biodiversity, biocapacity and better choices. http://wwf.panda.org/about_our_earth/all_publications/living_planet_report/2012_lpr/